TO THE CLAIMS:

Please amend the claims as indicated in the claim listing below.

Claims 1-19 (cancelled)

20. (currently amended) A method for identifying a gene associated with a detectable phenotype in a fungus, comprising:

(a) transforming the fungus with a polynucleotide comprising a marker gene which would otherwise be transcriptionally active in the fungus but which has been inactivated by the insertion of an *Impala* transposon, said marker gene comprising, in the direction of transcription, a promoter regulatory sequence of the niaD gene from *Aspergillus nidulans* which is more than 0.4 kb long and which is functionally linked to the coding sequence of said marker gene, under conditions in which transposase is expressed, which allow the excision of the *Impala* transposon from said marker gene and its reinsertion into the genome of the fungus;

(b) selecting at least one insertion mutant with said detectable phenotype; and

(c) isolating the gene into which, or close to which, the *Impala* transposon has inserted in the insertion mutant selected in (b).

21. (previously presented) The method of claim 20, wherein the marker gene is selected from the group consisting of a reporter gene, a gene that confers tolerance to an antibiotic, and a gene that confers tolerance to an herbicide.

22. (previously presented) The method of claim 21, wherein the marker gene is a reporter gene selected from the group consisting of glucuronidase and green fluorescent protein.

23. (previously presented) The method of claim 21, wherein the marker gene is a gene that confers tolerance to an antibiotic selected from the group consisting of hygromycin, phleomycin, and sulfonylurea.

24. (previously presented) The method of claim 21, wherein the marker gene is the gene that confers tolerance to the herbicide bialaphos.

25. (previously presented) The method of claim 20, wherein the marker gene encodes an enzyme that is active in the fungus.

26. (previously presented) The method of claim 25, wherein the marker gene encodes a nitrate reductase or a nitrilase.

27. (previously presented) The method of claim 26, wherein the marker gene is a nitrate reductase gene from *Aspergillus nidulans*.

28. (previously presented) The method of claim 20, 21, 22, 23, 24, 25, 26 or 27 wherein the *Impala* transposon is integrated into the promoter regulatory sequence.

29. (previously presented) The method of claim 28, wherein the *Impala* transposon carries an additional marker gene.

30. (currently amended) A method for identifying a gene associated with a detectable phenotype in a fungus, comprising:

(a) transforming the fungus with a polynucleotide comprising a marker gene which would otherwise be transcriptionally active in the fungus but which has been inactivated by the insertion of a ~~non-mobile~~ defective *Impala* transposon, said marker gene comprising, in the direction of transcription, a promoter regulatory sequence of the niaD gene from *Aspergillus*

nidulans which is more than 0.4 kb long and which is functionally linked to the coding sequence of said marker gene;

(b) mobilizing the ~~non-mobile~~ defective *Impala* transposon using a transposase, the expression of which is controlled, under conditions which allow the excision of the ~~defective~~ *Impala* transposon, and further controlling expression of the transposase so as to permit ~~its~~ reinsertion and ~~its~~ stabilization of the *Impala* transposon in the genome of the fungus;

(c) selecting at least one insertion mutant with said detectable phenotype; and

(d) isolating the gene into which, or close to which, the *Impala* transposon has inserted in the insertion mutant selected in (c).

31. (previously presented) The method of claim 30, wherein the marker gene encodes an enzyme that is active in the fungus.

32. (previously presented) The method of claim 31, wherein the marker gene encodes a nitrate reductase or a nitrilase.

33. (previously presented) The method of claim 32, wherein the marker gene is a nitrate reductase gene from *Aspergillus nidulans*.

34. (previously presented) The method of claim 30, 31, 32, or 33, wherein the *Impala* transposon is integrated into the promoter regulatory sequence.

35. (previously presented) The method of claim 34, wherein the *Impala* transposon carries an additional marker gene.